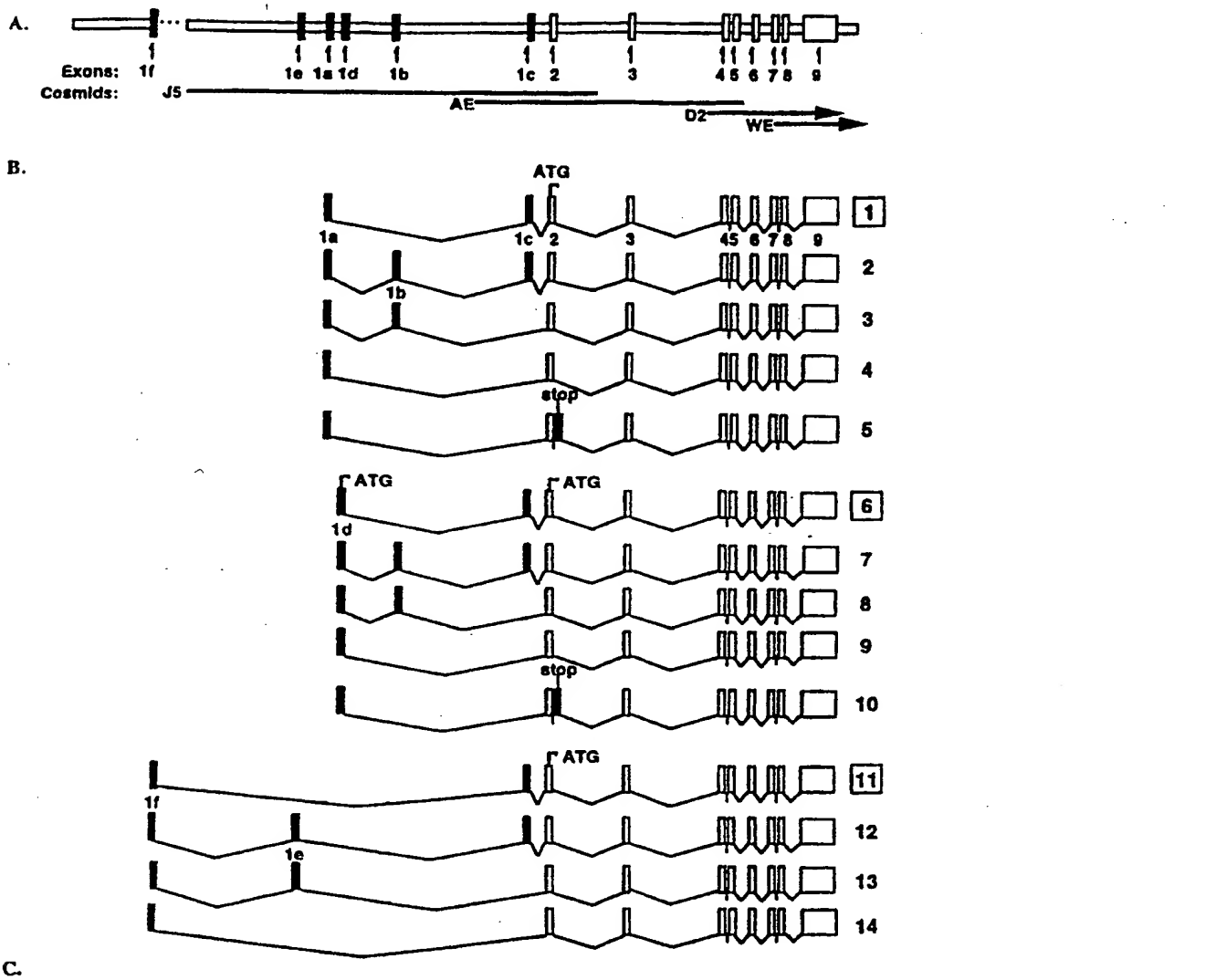
A.
Exons: 1f 1e 1a 1d 1b 1c 2 3 4 5 6 7 8 9
Cosmids: J5 AE D2 WE
B.
ATG
1a 1c 2 3 4 5 6 7 8 9
1
2
1b
3
4
stop
5
ATG ATG
1d
6
7
8
9
stop
10
ATG
1f
11
1e
12
13
14
C.
Transcript 1: MEAMA ASTSL PDPGD FDRNV PRI DBD 427aa
Transcript 6: MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPHR RAPLG STYLP PAPSG MEAMA ASTSL PDPGD FDRNV PRI DBD 477aa
Transcript 9: MEW RNKKR SDWLS MVLRT AGVEG MEAMA ASTSL PDPGD FDRNV PRI DBD 450aa

FIGURE 1

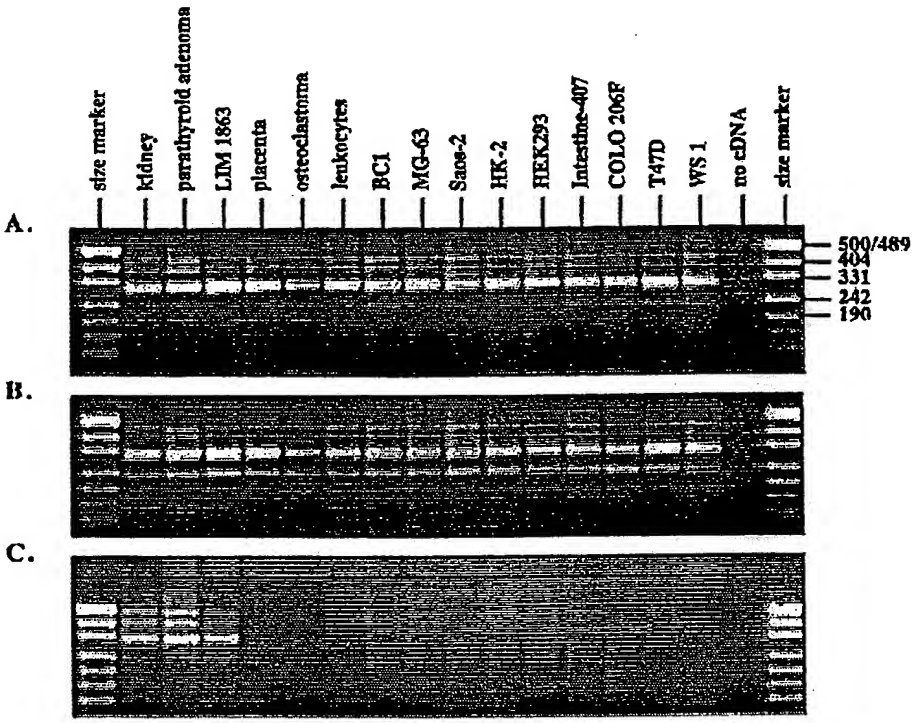
size marker
kidney
parathyroid adenoma
LIM 1863
placenta
osteoclastoma
leukocytes
BC1
MG-63
Saos-2
HK-2
HEK293
Intestine-407
COLO 206F
T47D
WS 1
no cDNA
size marker
A.
B.
C.
500/489
404
331
242
190

FIGURE 2

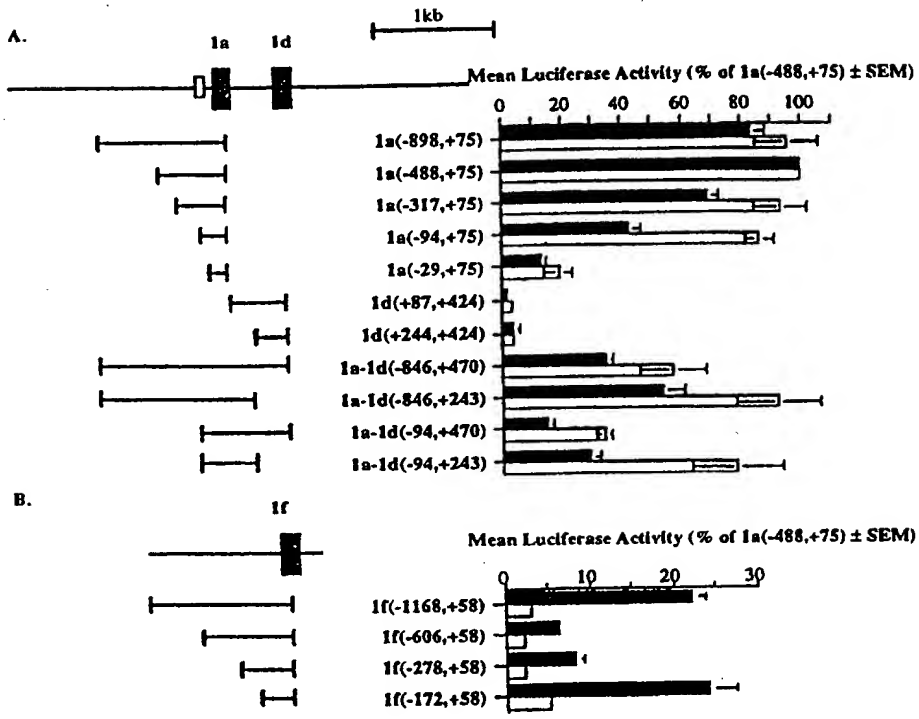
A.
1kb
1a
1d
Mean Luciferase Activity (% of 1a(-488,+75) ± SEM)
0
20
40
60
80
100
1a(-898,+75)
1a(-488,+75)
1a(-317,+75)
1a(-94,+75)
1a(-29,+75)
1d(+87,+424)
1d(+244,+424)
1a-1d(-846,+470)
1a-1d(-846,+243)
1a-1d(-94,+470)
1a-1d(-94,+243)
B.
1f
Mean Luciferase Activity (% of 1a(-488,+75) ± SEM)
0
10
20
30
1f(-1168,+58)
1f(-606,+58)
1f(-278,+58)
1f(-172,+58)

FIGURE 3

A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGCACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3'

B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGACGCAGGGGCCCGGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3'

C. 5'...tgttttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3'

D. 5'...GTTTCCTTCTTCTGTCGGGGCGCCTTGGCATGGAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTCGATGGTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3'

FIGURE 4

FIGURE 5 TRANSCRIPT 6

(Sequence Range: 1 to 1463)

```
          10         20         30         40         50
      *    *     *    *     *    *     *    *     *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                    MetGluTrpArg AsnLysLys>

          60         70         80         90         100
      *    *     *    *     *    *     *    *     *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

         110        120        130        140        150
      *    *     *    *     *    *     *    *     *    *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
 PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

         160        170        180        190        200
      *    *     *    *     *    *     *    *     *    *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

         210        220        230        240        250
      *    *     *    *     *    *     *    *     *    *
ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

         260        270        280        290        300
      *    *     *    *     *    *     *    *     *    *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
 GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

         310        320        330        340        350
      *    *     *    *     *    *     *    *     *    *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

         360        370        380        390        400
      *    *     *    *     *    *     *    *     *    *
TTCACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>
```

```
      410         420         430         440         450
    *   *   *   *   *   *   *   *   *   *
CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT
 HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

      460         470         480         490         500
    *   *   *   *   *   *   *   *   *   *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

      510         520         530         540         550
    *   *   *   *   *   *   *   *   *   *
CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
GACTTCGCCT TCCTCCTCCT CCGGAACTTC CTGTCAGACG CCGGGTTCGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

      560         570         580         590         600
    *   *   *   *   *   *   *   *   *   *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
 SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

      610         620         630         640         650
    *   *   *   *   *   *   *   *   *   *
AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

      660         670         680         690         700
    *   *   *   *   *   *   *   *   *   *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

      710         720         730         740         750
    *   *   *   *   *   *   *   *   *   *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
 ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

      760         770         780         790         800
    *   *   *   *   *   *   *   *   *   *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

      810         820         830         840         850
    *   *   *   *   *   *   *   *   *   *
AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>
```

```
      860        870        880        890        900
   *    *     *    *     *    *     *    *     *    *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC
 SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

      910        920        930        940        950
   *    *     *    *     *    *     *    *     *    *
TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

      960        970        980        990       1000
   *    *     *    *     *    *     *    *     *    *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

     1010       1020       1030       1040       1050
   *    *     *    *     *    *     *    *     *    *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
 SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

     1060       1070       1080       1090       1100
   *    *     *    *     *    *     *    *     *    *
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

     1110       1120       1130       1140       1150
   *    *     *    *     *    *     *    *     *    *
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

     1160       1170       1180       1190       1200
   *    *     *    *     *    *     *    *     *    *
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
 LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

     1210       1220       1230       1240       1250
   *    *     *    *     *    *     *    *     *    *
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

     1260       1270       1280       1290       1300
   *    *     *    *     *    *     *    *     *    *
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>
```

```
                                                1310        1320        1330        1340        1350
                                                 *   *       *   *       *   *       *   *       *   *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG
 GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

                1360        1370        1380        1390        1400
                 *   *       *   *       *   *       *   *       *   *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

                1410        1420        1430        1440        1450
                 *   *       *   *       *   *       *   *       *   *
CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

                1460
                 *   *
TGAGATCTCC TGA
ACTCTAGAGG ACT
 GluIleSer ***>
```

FIGURE 6 TRANSCRIPT 9

(Sequence Range: 1 to 1382)

```
          10        20        30        40        50
          *    *    *    *    *    *    *    *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                  MetGluTrpArg AsnLysLys>

          60        70        80        90       100
          *    *    *    *    *    *    *    *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

         110       120       130       140       150
          *    *    *    *    *    *    *    *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

         160       170       180       190       200
          *    *    *    *    *    *    *    *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

         210       220       230       240       250
          *    *    *    *    *    *    *    *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

         260       270       280       290       300
          *    *    *    *    *    *    *    *    *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

         310       320       330       340       350
          *    *    *    *    *    *    *    *    *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

         360       370       380       390       400
          *    *    *    *    *    *    *    *    *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>
```

```
       410         420         430         440         450
   *   *   *   *   *   *   *   *   *   *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACTTCC
 ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

       460         470         480         490         500
   *   *   *   *   *   *   *   *   *   *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

       510         520         530         540         550
   *   *   *   *   *   *   *   *   *   *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

       560         570         580         590         600
   *   *   *   *   *   *   *   *   *   *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
 GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

       610         620         630         640         650
   *   *   *   *   *   *   *   *   *   *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

       660         670         680         690         700
   *   *   *   *   *   *   *   *   *   *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

       710         720         730         740         750
   *   *   *   *   *   *   *   *   *   *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
 PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

       760         770         780         790         800
   *   *   *   *   *   *   *   *   *   *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

       810         820         830         840         850
   *   *   *   *   *   *   *   *   *   *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCGT AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>
```

```
      860        870        880        890        900
    *   *      *   *      *   *      *   *      *   *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
 ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

      910        920        930        940        950
    *   *      *   *      *   *      *   *      *   *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

      960        970        980        990       1000
    *   *      *   *      *   *      *   *      *   *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

     1010       1020       1030       1040       1050
    *   *      *   *      *   *      *   *      *   *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
 LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

     1060       1070       1080       1090       1100
    *   *      *   *      *   *      *   *      *   *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

     1110       1120       1130       1140       1150
    *   *      *   *      *   *      *   *      *   *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

     1160       1170       1180       1190       1200
    *   *      *   *      *   *      *   *      *   *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
 IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

     1210       1220       1230       1240       1250
    *   *      *   *      *   *      *   *      *   *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

     1260       1270       1280       1290       1300
    *   *      *   *      *   *      *   *      *   *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>
```

```
                1310        1320        1330        1340        1350
                 *   *       *   *       *   *       *   *       *   *
CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC
 ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

                1360        1370        1380
                 *   *       *   *       *   *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT
ValLeuGluVal PheGlyAsn GluIleSer ***>
```

FIGURE 7 TRANSCRIPT 10

(Sequence Range: 1 to 1534)

```
                10         20         30         40         50
         *      *    *     *    *     *    *     *    *     *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                 MetGluTrpArg AsnLysLys>

                60         70         80         90        100
         *      *    *     *    *     *    *     *    *     *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

               110        120        130        140        150
         *      *    *     *    *     *    *     *    *     *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

               160        170        180        190        200
         *      *    *     *    *     *    *     *    *     *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

               210        220        230        240        250
         *      *    *     *    *     *    *     *    *     *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***

               260        270        280        290        300
         *      *    *     *    *     *    *     *    *     *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC

               310        320        330        340        350
         *      *    *     *    *     *    *     *    *     *
TTTCCATGAA GGGAGCCCTT GCATTTTTCA CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

               360        370        380        390        400
         *      *    *     *    *     *    *     *    *     *
CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT
```

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                410       420       430       440       450
                *   *     *   *     *   *     *   *     *   *
AGCATGAAGC GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC

                460       470       480       490       500
                *   *     *   *     *   *     *   *     *   *
CATCACCAAG GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA

                510       520       530       540       550
                *   *     *   *     *   *     *   *     *   *
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC

                560       570       580       590       600
                *   *     *   *     *   *     *   *     *   *
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT

                610       620       630       640       650
                *   *     *   *     *   *     *   *     *   *
GGACAGTCTG CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT

                660       670       680       690       700
                *   *     *   *     *   *     *   *     *   *
TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG

                710       720       730       740       750
                *   *     *   *     *   *     *   *     *   *
TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
ACGGTCAAGG CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG

                760       770       780       790       800
                *   *     *   *     *   *     *   *     *   *
TTCCAGGCCC AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA

                810       820       830       840       850
                *   *     *   *     *   *     *   *     *   *
CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG

                860       870       880       890       900
                *   *     *   *     *   *     *   *     *   *
AGCTTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT
TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA

                910       920       930       940       950
                *   *     *   *     *   *     *   *     *   *
GACCCTAGAG CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC
```

```
      960        970        980        990       1000
   *    *     *    *     *    *     *    *     *    *
TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
AGTCAATGTC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT

     1010       1020       1030       1040       1050
   *    *     *    *     *    *     *    *     *    *
TTCAGAGACC TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC
AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG

     1060       1070       1080       1090       1100
   *    *     *    *     *    *     *    *     *    *
CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
GTAACTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT

     1110       1120       1130       1140       1150
   *    *     *    *     *    *     *    *     *    *
TGTCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC

     1160       1170       1180       1190       1200
   *    *     *    *     *    *     *    *     *    *
ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT

     1210       1220       1230       1240       1250
   *    *     *    *     *    *     *    *     *    *
GGTGGGACTG AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA
CCACCCTGAC TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT

     1260       1270       1280       1290       1300
   *    *     *    *     *    *     *    *     *    *
TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC

     1310       1320       1330       1340       1350
   *    *     *    *     *    *     *    *     *    *
CTGATTGAGG CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT
GACTAACTCC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA

     1360       1370       1380       1390       1400
   *    *     *    *     *    *     *    *     *    *
CCGCTGCCGC CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
GGCGACGGCG GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT

     1410       1420       1430       1440       1450
   *    *     *    *     *    *     *    *     *    *
TCCAGAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
AGGTCTTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC

     1460       1470       1480       1490       1500
   *    *     *    *     *    *     *    *     *    *
TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT
ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA
```

```
          1510        1520        1530
           *   *       *   *       *   *
TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT
```

FIGURE 8 TRANSCRIPT 11

```
        10          20          30          40          50
         *           *           *           *           *
TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC

        60          70          80          90          100
         *           *           *           *           *
GACGCAGGGG CCCGGCCCAA GGCGAGGGAG AACAGCGGCA CTAAGGCAGA
CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT

        110         120         130         140         150
         *           *           *           *           *
AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG

        160         170         180         190         200
         *           *           *           *           *
TCCTAGACGC TGGTAGAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG
AGGATCTGCG ACCATCTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC

        210         220         230         240         250
         *           *           *           *           *
CGTGCAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG

        260         270         280         290         300
         *           *           *           *           *
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
                                            MetGluAla>

        310         320         330         340         350
         *           *           *           *           *
TGGCGGCCAG CACTTCCCTG CCTGACCCTG GAGACTTTGA CCGGAACGTG
ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTGCAC
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>

        360         370         380         390         400
         *           *           *           *           *
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
GGGGCCTAGA CACCCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>

        410         420         430         440         450
         *           *           *           *           *
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAGGCGA AGCATGAAGC
ACGATACTGG ACACTTCCGA CGTTTCCGAA GAAGTCCGCT TCGTACTTCG
 AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>

        460         470         480         490         500
         *           *           *           *           *
GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG CATCACCAAG
CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC GTAGTGGTTC
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>
```

```
       510         520         530         540         550
        *           *           *           *           *
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

       560         570         580         590         600
        *           *           *           *           *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
 GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

       610         620         630         640         650
        *           *           *           *           *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT CCTGTCAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

       660         670         680         690         700
        *           *           *           *           *
CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

       710         720         730         740         750
        *           *           *           *           *
CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
 AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

       760         770         780         790         800
        *           *           *           *           *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

       810         820         830         840         850
        *           *           *           *           *
AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

       860         870         880         890         900
        *           *           *           *           *
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
 AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

       910         920         930         940         950
        *           *           *           *           *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

       960         970         980         990        1000
        *           *           *           *           *
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>
```

```
                1010        1020        1030        1040        1050
                 *           *           *           *           *
CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
 IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

      1060        1070        1080        1090        1100
       *           *           *           *           *
TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

      1110        1120        1130        1140        1150
       *           *           *           *           *
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC
TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

      1160        1170        1180        1190        1200
       *           *           *           *           *
CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
 CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

      1210        1220        1230        1240        1250
       *           *           *           *           *
GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

      1260        1270        1280        1290        1300
       *           *           *           *           *
AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

      1310        1320        1330        1340        1350
       *           *           *           *           *
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC
 IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

      1360        1370        1380        1390        1400
       *           *           *           *           *
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

      1410        1420        1430        1440        1450
       *           *           *           *           *
CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

      1460        1470        1480        1490        1500
       *           *           *           *           *
AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
 AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
```

```
      1510        1520        1530        1540        1550
        *           *           *           *           *
TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA
AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

      1560        1570
        *           *
GTGTTTGGCA ATGAGATCTC CTGA
CACAAACCGT TACTCTAGAG GACT
ValPheGly AsnGluIleSer ***>
```